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# Macrogeographic population structuring in the cosmopolitan agricultural pest Bactrocera cucurbitae (Diptera: Tephritidae)

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Background: The melon fly Bactrocera cucurbitae (Coquillett) is a major, highly polyphagous, agricultural pest abundant throughout the African continent, the islands of Indian Ocean, Asia, New Guinea, the Mariana Islands and Hawaii. This species attacks more than 125 plants including commercial crops such as pumpkin, cantaloupe, watermelon, squash, gourd, cucumber, tomato, eggplant and bean as well as soft fruits such as mango, orange, papaya and peach. Although the economic importance of B. cucurbitae is well documented, its large-scale (i.e. inter-regional) patterns of genetic structuring are poorly known. Hence, the current quarantine methods and management plans still rely on general assumptions concerning its intraspecific variation. The aim of this work was to 1) characterize the large-scale population structure of Bactrocera cucurbitae, 2) identify its geographic origin and 3) infer the dynamics of its range expansion.
Methods: Individuals of B. cucurbitae were collected from 25 worldwide-distributed localities (n=570) and genotyped at 13 microsatellite loci specifically developed for this species. Genetic discontinuities among geographical regions were quantified through hierarchical analysis of molecular variance (AMOVA) and levels of population admixture were quantified through Bayesian clustering procedures
Results: Five main groups of populations were identified. These corresponded to populations from 1) the African continent, 2) La Réunion, 3) Central Asia, 4) East Asia and 5) Hawaii. The proportions of inter-regional assignments and the higher values of genetic diversity in populations from Pakistan, India and Bangladesh suggest that B. cucurbitae originated in Central Asia and expanded its range to East Asia and Hawaii on one hand and to Africa and the islands of the Indian Ocean on the other. A number of outliers (10-19 specimens according to different clustering algorithms) show high levels of admixture (Q>0.70) with populations from different regions and reveal complex patterns of inter-regional gene flow.
Conclusions: Anthropogenic transport is the most plausible promoter of the large-scale dispersal of B. cucurbitae. The recent African invasions of B. cucurbitae were mainly due to the expansion of local populations while, hitherto, the introduction of individuals from geographically distant regions did not have a relevant role. The dynamics of the recent invasions, as well as the possible corridors to gene flow created by contemporary anthropogenic activities could provide a useful background to better evaluate invasion risks and establish priorities for the management of this cosmopolitan agricultural pest.

Key words: Tephritidae, agricultural pests, biological invasions, population structure, microsatellites.